

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/584,886  
Source: TFW0  
Date Processed by STIC: 11/09/2006

# ***ENTERED***



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## RAW SEQUENCE LISTING

DATE: 11/09/2006

PATENT APPLICATION: US/10/584,886

TIME: 13:00:58

Input Set: N:\efs\10584886\_efs\Sequence\_List\_176\_61623.txt

Output Set: N:\CRF4\11092006\J584886.raw

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3 <110> APPLICANT: Maines, Mahin D.
5 <120> TITLE OF INVENTION: METHODS OF MODULATING CELL CYCLE AND CELL SIGNALING PATHWAYS
6     USING BILIVERDIN REDUCTASE
8 <130> FILE REFERENCE: 176/61623 (1208)
10 <140> CURRENT APPLICATION NUMBER: 10/584,886
C--> 11 <141> CURRENT FILING DATE: 2006-06-29
13 <150> PRIOR APPLICATION NUMBER: PCT/US2004/031866
14 <151> PRIOR FILING DATE: 2004-09-29
16 <150> PRIOR APPLICATION NUMBER: 60/539,006
17 <151> PRIOR FILING DATE: 2004-09-29
19 <150> PRIOR APPLICATION NUMBER: 60/506,805
20 <151> PRIOR FILING DATE: 2003-09-29
22 <160> NUMBER OF SEQ ID NOS: 7
24 <170> SOFTWARE: PatentIn version 3.3
26 <210> SEQ ID NO: 1
28 <400> SEQUENCE: 1
W--> 29 000
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 1070
33 <212> TYPE: DNA
34 <213> ORGANISM: Human BVR
36 <400> SEQUENCE: 2
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39 atgaatgcag agcccagagag gaagtttggtc gtggtggtgg ttggtggtgg ccgagccggc      120
41 tccgtgcgga tgagggactt gcggaatcca cacccttcct cagcgttcct gaacctgatt      180
43 ggcttcgtgt cgagaaggga gtcgaggagc attgatggag tccagcagat ttctttggag      240
45 gatgctcttt ccagccaaga ggtggagggt gcctatatct gcagtgagag ctccagccat      300
47 gaggactaca tcaggcagtt ccttaatgct ggcaagcacg tccttggtga ataccccatg      360
49 aactgtcat tggcgccgcgc tcaggaactg tgggagctgg ctgagcagaa aggaaaagtc      420
51 ttgcacgagg agcatgttga actcttgatg gaggaattcg ctttcctgaa aaaagaagtg      480
53 gtggggaaaag acctgctgaa agggctcgtc ctcttcacat ctgaccggtt ggaagaagac      540
55 cggtttggtt tccctgcatt cagcggcatc tctcgactga cctggctggt ctccctcttt      600
57 ggggagcttt ctcttggtgc tgccactttg gaagagcgaa aggaagatca gtatatgaaa      660
59 atgacagtgt gtctggagac agagaagaaa agtccactgt catggattga agaaaaagga      720
61 cctggtctaa aacgaaacag atatttaagc ttccatttca agtctgggtc cttggagaat      780
63 gtgccaaatg taggagtga taagaacata tttctgaaag atcaaaatat atttgtccag      840
65 aaactcttgg gccagttctc tgagaaggaa ctggctgctg aaaagaaacg catcctgcac      900
67 tgcctggggc ttgcagaaga aatccagaaa tattgctgtt caaggaagta agaggaggag      960
69 gtgatgtagc acttccaaga tggcaccagc atttggttct tctcaagagt tgaccattat     1020
71 ctctattctt aaaattaaac atgttgggga aacaaaaaaaa aaaaaaaaaa     1070
74 <210> SEQ ID NO: 3
75 <211> LENGTH: 296
76 <212> TYPE: PRT

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77 &lt;213&gt; ORGANISM: Human BVR

79 &lt;400&gt; SEQUENCE: 3

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81 Met Asn Thr Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
82 1          5          10          15
85 Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
86          20          25          30
89 Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
90          35          40          45
93 Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
94          50          55          60
97 Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
98 65          70          75          80
101 Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
102          85          90          95
105 Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
106          100          105          110
109 Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
110          115          120          125
113 Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
114          130          135          140
117 Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu Glu
118 145          150          155          160
121 Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
122          165          170          175
125 Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
126          180          185          190
129 Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
130          195          200          205
133 Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
134          210          215          220
137 Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
138 225          230          235          240
141 Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
142          245          250          255
145 Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
146          260          265          270
149 Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
150          275          280          285
153 Gln Lys Tyr Cys Cys Ser Arg Lys
154          290          295

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157 &lt;210&gt; SEQ ID NO: 4

158 &lt;211&gt; LENGTH: 295

159 &lt;212&gt; TYPE: PRT

160 &lt;213&gt; ORGANISM: Rat BVR

162 &lt;400&gt; SEQUENCE: 4

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164 Met Asp Ala Glu Pro Lys Arg Lys Phe Gly Val Val Val Val Gly Val
165 1          5          10          15
168 Gly Arg Ala Gly Ser Val Arg Leu Arg Asp Leu Lys Asp Pro Arg Ser
169          20          25          30

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172 Ala Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu Gly
173      35                        40                        45
176 Ser Leu Asp Glu Val Arg Gln Ile Ser Leu Glu Asp Ala Leu Arg Ser
177      50                        55                        60
180 Gln Glu Ile Asp Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His Glu
181 65                        70                        75                        80
184 Asp Tyr Ile Arg Gln Phe Leu Gln Ala Gly Lys His Val Leu Val Glu
185      85                        90                        95
188 Tyr Pro Met Thr Leu Ser Phe Ala Ala Ala Gln Glu Leu Trp Glu Leu
189      100                       105                       110
192 Ala Ala Gln Lys Gly Arg Val Leu His Glu Glu His Val Glu Leu Leu
193      115                       120                       125
196 Met Glu Glu Phe Glu Phe Leu Arg Arg Glu Val Leu Gly Lys Glu Leu
197      130                       135                       140
200 Leu Lys Gly Ser Leu Arg Phe Thr Ala Ser Pro Leu Glu Glu Glu Arg
201 145                       150                       155                       160
204 Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu Val
205      165                       170                       175
208 Ser Leu Phe Gly Glu Leu Ser Leu Ile Ser Ala Thr Leu Glu Glu Arg
209      180                       185                       190
212 Lys Glu Asp Gln Tyr Met Lys Met Thr Val Gln Leu Glu Thr Gln Asn
213      195                       200                       205
216 Lys Gly Leu Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys Arg
217      210                       215                       220
220 Asn Arg Tyr Val Asn Phe Gln Phe Thr Ser Gly Ser Leu Glu Glu Val
221 225                       230                       235                       240
224 Pro Ser Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asp Ile
225      245                       250                       255
228 Phe Val Gln Lys Leu Leu Asp Gln Val Ser Ala Glu Asp Leu Ala Ala
229      260                       265                       270
232 Glu Lys Lys Arg Ile Met His Cys Leu Gly Leu Ala Ser Asp Ile Gln
233      275                       280                       285
236 Lys Leu Cys His Gln Lys Lys
237      290                       295
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241 <211> LENGTH: 1081
242 <212> TYPE: DNA
243 <213> ORGANISM: Rat BVR
245 <400> SEQUENCE: 5
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248 aacctctgtc tgtcttcgga cactgactga agagaccgag atggatgccg agccaaagag      120
250 gaaatttgga gtggtagtgg ttggtgttgg cagagctggc tcggtgaggc tgagggactt      180
252 gaaggatcca cgctctgcag cattcctgaa cctgattgga tttgtgtcca gacgagagct      240
254 tgggagcctt gatgaagtac ggcagatttc tttggaagat gctctccgaa gccaaagat      300
256 tgatgtcgcc tatatttgca gtgagagttc cagccatgaa gactatatac ggcagtttct      360
258 gcaggctggc aagcatgtcc tcgtggaata ccccatgaca ctgtcatttg cggcggccca      420
260 ggagctgtgg gagctggccg cacagaaagg gagagtcttg catgaggagc acgtggaact      480
262 cttgatggag gaattcgaat tcctgagaag agaagtgttg gggaaagagc tactgaaagg      540
264 gtctcttcgc ttcacagcta gccactgga agaagagaga tttggcttcc ctgcgttcag      600

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266 cggcattttct cgcttgacct ggctgggtctc cctcttcggg gagctttctc ttattttctgc      660
268 caccttggaag gagcgaaaag aggatcagta tatgaaaatg accgtgcagc tggagaccca      720
270 gaacaagggt ctgctgtcat ggattgaaga gaaagggcct ggcttaaaaa gaaacagata      780
272 tgtaaaacttc cagttcactt ctgggtccct ggaggaagtg ccaagtgtag ggggtcaataa      840
274 gaacatttttc ctgaaagatc aggatataatt tgttcagaag ctcttagacc aggtctctgc      900
276 agaggacctg gctgctgaga agaagcgcac catgcattgc ctggggctgg ccagcgacat      960
278 ccagaagctt tgccaccaga agaagtgaag aggaagcttc agagacttct gaagggggcc     1020
280 agggtttggt cctatcaacc attcaccttt agctcttaca attaaacatg tcagataaac     1080
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285 <210> SEQ ID NO: 6
286 <211> LENGTH: 295
287 <212> TYPE: PRT
288 <213> ORGANISM: Mouse BVR
290 <400> SEQUENCE: 6
292 Met Ser Thr Glu Pro Lys Arg Lys Phe Gly Val Val Val Val Gly Val
293 1                    5                    10                    15
296 Gly Arg Ala Gly Ser Val Arg Ile Arg Asp Ser Lys Asp Pro His Ser
297                20                    25                    30
300 Ser Ala Phe Leu Asn Leu Ile Gly Tyr Val Ser Arg Arg Glu Leu Gly
301                35                    40                    45
304 Ser Leu Asp Asn Val Arg Gln Ile Ser Leu Glu Asp Ala Leu Arg Ser
305                50                    55                    60
308 Gln Glu Val Asp Val Ala Tyr Ile Cys Thr Glu Ser Ser Ser His Glu
309 65                70                    75                    80
312 Asp Tyr Ile Arg Gln Phe Leu Gln Ala Gly Lys His Val Leu Val Glu
313                85                    90                    95
316 Tyr Pro Met Ala Leu Ser Phe Ala Ala Ala Gln Glu Leu Trp Glu Leu
317                100                   105                   110
320 Ala Ala Gln Lys Gly Arg Val Leu His Glu Glu His Ile Glu Leu Leu
321                115                   120                   125
324 Met Glu Glu Phe Glu Phe Leu Lys Arg Glu Val Ala Gly Lys Glu Leu
325                130                   135                   140
328 Leu Lys Gly Ser Leu Arg Phe Thr Ala Ser Pro Leu Glu Glu Glu Lys
329 145                150                   155                   160
332 Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu Val
333                165                   170                   175
336 Ser Leu Phe Gly Glu Leu Ser Leu Ile Ser Ala Thr Met Glu Asn Arg
337                180                   185                   190
340 Lys Glu Asp Gln Tyr Met Lys Met Thr Val Gln Leu Glu Thr Gln Asn
341                195                   200                   205
344 Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys Arg
345                210                   215                   220
348 Asn Arg His Ile Ser Ile His Phe Lys Ser Gly Ser Leu Glu Glu Val
349 225                230                   235                   240
352 Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asp Ile
353                245                   250                   255
356 Phe Ile Gln Lys Leu Leu Gly Gln Val Ser Ala Glu Asp Leu Ala Ala
357                260                   265                   270
360 Glu Lys Lys Arg Ile Leu His Cys Leu Glu Leu Ala Ser Asp Ile Gln

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364 Arg Leu Cys His Arg Lys Gln
365          290          295
368 <210> SEQ ID NO: 7
369 <211> LENGTH: 296
370 <212> TYPE: PRT
371 <213> ORGANISM: Pig BVR
373 <400> SEQUENCE: 7
375 Met Asn Ala Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
376 1          5          10          15
379 Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
380          20          25          30
383 Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
384          35          40          45
387 Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
388          50          55          60
391 Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
392 65          70          75          80
395 Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
396          85          90          95
399 Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
400          100         105         110
403 Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
404          115         120         125
407 Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
408          130         135         140
411 Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu Glu
412 145         150         155         160
415 Arg Phe Gly Ser Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
416          165         170         175
419 Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
420          180         185         190
423 Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
424          195         200         205
427 Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
428          210         215         220
431 Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
432 225         230         235         240
435 Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
436          245         250         255
439 Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
440          260         265         270
443 Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
444          275         280         285
447 Gln Lys Tyr Cys Cys Ser Arg Lys
448          290         295

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/584,886

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Input Set : N:\efs\10584886\_efs\Sequence\_List\_176\_61623.txt

Output Set: N:\CRF4\11092006\J584886.raw

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